

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/563,503A
Source: 1Fu0
Date Processed by STIC: 6/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/563,503A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics <input checked="" type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned: Do not use tab codes between numbers; use space characters , instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input checked="" type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input checked="" type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:11

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

5 <110> APPLICANT: Stordeur, Patrick
6 Goldman, Michel
10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and

11 stabilising the sample so pulsed
15 <130> FILE REFERENCE: DECLE35.005APC
19 <140> CURRENT APPLICATION NUMBER: 10/563,503A
20 <141> CURRENT FILING DATE: 2006-01-04
22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
23 <151> PRIOR FILING DATE: 2003-07-10
26 <160> NUMBER OF SEQ ID NOS: 10
28 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
Corrected Diskette Needed

pp1-2

32 <210> SEQ ID NO: 1
34 <211> LENGTH: 22
36 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens

22

42 <400> SEQUENCE: 1
43 ctaccaggta tgctcacatt ta
44 <210> SEQ ID NO: 2
46 <211> LENGTH: 24
48 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens

24

54 <400> SEQUENCE: 2
55 tccagagggt tgagttcttc ttct
56 <210> SEQ ID NO: 3
58 <211> LENGTH: 25

24

60 <212> TYPE: DNA
62 <213> ORGANISM: Homo sapiens
66 <220> FEATURE:

"n" can only represent a nucleotide,
not a label or
dye.

68 <221> NAME/KEY: misc_feature
70 <222> LOCATION: (1)..(1)

6Fam

72 <223> OTHER INFORMATION: N = 6Fam
75 <220> FEATURE:

77 <221> NAME/KEY: misc_feature
79 <222> LOCATION: (25)..(25)

(25)

81 <223> OTHER INFORMATION: N = Tamra-p
84 <400> SEQUENCE: 3

25

W--> 85 ntgccaaga aggccacaga actgn

86 <210> SEQ ID NO: 4
88 <211> LENGTH: 21

21

90 <212> TYPE: DNA
92 <213> ORGANISM: Homo sapiens

96 <400> SEQUENCE: 4
97 actttgaaca gcctcacaga g

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006

TIME: 09:50:11

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06142006\J563503A.raw

98 <210> SEQ ID NO: 5
 100 <211> LENGTH: 20
 102 <212> TYPE: DNA
 104 <213> ORGANISM: Homo sapiens
 108 <400> SEQUENCE: 5
 109 ttggaggcag caaagatgtc 20
 110 <210> SEQ ID NO: 6
 112 <211> LENGTH: 23
 114 <212> TYPE: DNA
 116 <213> ORGANISM: Homo sapiens
 120 <220> FEATURE:
 122 <221> NAME/KEY: misc_feature
 124 <222> LOCATION: (1)..(1)
 126 <223> OTHER INFORMATION: N - 6Fam
 129 <220> FEATURE:
 131 <221> NAME/KEY: misc_feature
 133 <222> LOCATION: (23)..(23)
 135 <223> OTHER INFORMATION: N = Tamra-p
 138 <400> SEQUENCE: 6
 W--> 139 nctgtgcacc gagttgaccg tan 23
 140 <210> SEQ ID NO: 7
 142 <211> LENGTH: 22
 144 <212> TYPE: DNA
 146 <213> ORGANISM: Homo sapiens
 150 <400> SEQUENCE: 7
 151 tgtcacaaac agtgcaccta ct 22
 152 <210> SEQ ID NO: 8
 154 <211> LENGTH: 26
 156 <212> TYPE: DNA
 158 <213> ORGANISM: Homo sapiens
 162 <400> SEQUENCE: 8
 163 agttacaata ggttagcaaac cataca 26
 164 <210> SEQ ID NO: 9
 166 <211> LENGTH: 21
 168 <212> TYPE: DNA
 170 <213> ORGANISM: Homo sapiens
 174 <400> SEQUENCE: 9
 175 taattgcctc acattgtcac t 21
 176 <210> SEQ ID NO: 10
 178 <211> LENGTH: 21
 180 <212> TYPE: DNA
 182 <213> ORGANISM: Homo sapiens
 186 <400> SEQUENCE: 10
 187 attcagctcg aacactttga a 21

*Same char
as p. 1*

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A TIME: 09:50:12

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25
Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006

TIME: 09:50:12

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06142006\J563503A.raw

L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0

L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0